

Re-run

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 09/709,020A

Source: IFWO

Date Processed by STIC: 04/11/2007

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IFWO

## RAW SEQUENCE LISTING

DATE: 04/11/2007

PATENT APPLICATION: US/09/709,020A

TIME: 09:56:48

Input Set : A:\ES.txt

Output Set: N:\CRF4\04102007\I709020A.raw

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3 <110> APPLICANT: Benning, Christoph
4   Sanda, Sherrie
5   Yu, Bin
7 <120> TITLE OF INVENTION: Compositions and Methods for the Synthesis and Subsequent
Modification of
8   Uridine-5-Diphosphosulfoquinovose (UDP-SQ)
10 <130> FILE REFERENCE: MSU-04769
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/709,020A
C--> 12 <141> CURRENT FILING DATE: 2000-11-08
12 <160> NUMBER OF SEQ ID NOS: 24
14 <170> SOFTWARE: PatentIn version 3.0
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 1134
18 <212> TYPE: DNA
19 <213> ORGANISM: Cyanobacterium Synechococcus
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22 <221> NAME/KEY: CDS
23 <222> LOCATION: (1)..(1134)
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28 1           5           10           15
30 atc gtc acg cgg ctt cgg cac acg gtc gat cac ctg cag cgt ctt ggc      96
31 Ile Val Thr Arg Leu Arg His Thr Val Asp His Leu Gln Arg Leu Gly
32           20           25           30
34 cac acc gtc atg gtt ttt tgc ccc gac ggc ggg ctc cgc gag cac aag      144
35 His Thr Val Met Val Phe Cys Pro Asp Gly Gly Leu Arg Glu His Lys
36           35           40           45
38 ggg gct cga gtc tat ggg gtt aaa ggc ttt ccg cta ccg ctc tat ccc      192
39 Gly Ala Arg Val Tyr Gly Val Lys Gly Phe Pro Leu Pro Leu Tyr Pro
40           50           55           60
42 gag ctg aag cta gct ttt ccg ttg ccg aaa gtg gga aaa gcc ttg gag      240
43 Glu Leu Lys Leu Ala Phe Pro Leu Pro Lys Val Gly Lys Ala Leu Glu
44 65           70           75           80
46 cgg ttc cgg ccc gac ctg atc cac gtg gtc aat ccg gct gtg ttg ggg      288
47 Arg Phe Arg Pro Asp Leu Ile His Val Val Asn Pro Ala Val Leu Gly
48           85           90           95
50 ttg ggc ggc atc tac tat gcc aag gcg cta aat gtg cca ctc gtg gcg      336
51 Leu Gly Gly Ile Tyr Tyr Ala Lys Ala Leu Asn Val Pro Leu Val Ala
52           100          105          110
54 tcc tat cac acc cat ttg ccg aaa tac ctt gag cat tac ggg ctg ggg      384
55 Ser Tyr His Thr His Leu Pro Lys Tyr Leu Glu His Tyr Gly Leu Gly
56           115          120          125
58 gtc ttg gag ggg gtg ctc tgg gaa ttg ctg aag ctg gcg cat aac caa      432

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60      130      135      140
62 gca gcg atc aac ctc tgt act tca acc gcg atg gtg cag gag ctg aca      480
63 Ala Ala Ile Asn Leu Cys Thr Ser Thr Ala Met Val Gln Glu Leu Thr
64 145      150      155      160
66 gat cac ggc att gag cac tgt tgc ctc tgg cag cga gga gtg gat acc      528
67 Asp His Gly Ile Glu His Cys Cys Leu Trp Gln Arg Gly Val Asp Thr
68      165      170      175
70 gag acc ttt cgg cca gac ttg gct act gct gcg atg cgc gat cgc ctc      576
71 Glu Thr Phe Arg Pro Asp Leu Ala Thr Ala Ala Met Arg Asp Arg Leu
72      180      185      190
74 agt ggc ggt aag ccc act gcg ccc ttg ttg ctc tac gtc gga cgc ctc      624
75 Ser Gly Gly Lys Pro Thr Ala Pro Leu Leu Leu Tyr Val Gly Arg Leu
76      195      200      205
78 tca gcc gag aag caa atc gat cgc ctg cga ccc att ttg gat gcc aat      672
79 Ser Ala Glu Lys Gln Ile Asp Arg Leu Arg Pro Ile Leu Asp Ala Asn
80      210      215      220
82 cct gag gct tgc ttg gcc ttg gtc ggc gat ggc ccg cat cgg gcc gaa      720
83 Pro Glu Ala Cys Leu Ala Leu Val Gly Asp Gly Pro His Arg Ala Glu
84 225      230      235      240
86 cta gag caa ttg ttt gct ggc acc cag acg cag ttc att ggc tat ctg      768
87 Leu Glu Gln Leu Phe Ala Gly Thr Gln Thr Gln Phe Ile Gly Tyr Leu
88      245      250      255
90 cat ggg gaa cag cta ggg gcg gcc tac gct tct gct gac gct ttt gtc      816
91 His Gly Glu Gln Leu Gly Ala Ala Tyr Ala Ser Ala Asp Ala Phe Val
92      260      265      270
94 ttt ccc tcc cgg acc gaa acc ctc ggt cta gtc ttg ctg gaa gcc atg      864
95 Phe Pro Ser Arg Thr Glu Thr Leu Gly Leu Val Leu Leu Glu Ala Met
96      275      280      285
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100      290      295      300
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103 Ile Val Ser Asp Gly Ile Asn Gly Phe Leu Phe Asp Pro Glu Asp Glu
104 305      310      315      320
106 caa ggg gcg atc gct gcg att cag cgc ttg ttg gct aac cct gca gag      1008
107 Gln Gly Ala Ile Ala Ala Ile Gln Arg Leu Leu Ala Asn Pro Ala Glu
108      325      330      335
110 cgc gag att cta cgc caa gcg gct cgt caa gaa gcc gaa cgc tgg agc      1056
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112      340      345      350
114 tgg aac gca gcc acg cgc caa ctc cag gac tac tac tgc gag gtg ttg      1104
115 Trp Asn Ala Ala Thr Arg Gln Leu Gln Asp Tyr Tyr Cys Glu Val Leu
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120      370      375
123 <210> SEQ ID NO: 2
124 <211> LENGTH: 377

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126 <213> ORGANISM: Cyanobacterium Synechococcus
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135 20 25 30
138 His Thr Val Met Val Phe Cys Pro Asp Gly Gly Leu Arg Glu His Lys
139 35 40 45
142 Gly Ala Arg Val Tyr Gly Val Lys Gly Phe Pro Leu Pro Leu Tyr Pro
143 50 55 60
146 Glu Leu Lys Leu Ala Phe Pro Leu Pro Lys Val Gly Lys Ala Leu Glu
147 65 70 75 80
150 Arg Phe Arg Pro Asp Leu Ile His Val Val Asn Pro Ala Val Leu Gly
151 85 90 95
154 Leu Gly Gly Ile Tyr Tyr Ala Lys Ala Leu Asn Val Pro Leu Val Ala
155 100 105 110
158 Ser Tyr His Thr His Leu Pro Lys Tyr Leu Glu His Tyr Gly Leu Gly
159 115 120 125
162 Val Leu Glu Gly Val Leu Trp Glu Leu Leu Lys Leu Ala His Asn Gln
163 130 135 140
166 Ala Ala Ile Asn Leu Cys Thr Ser Thr Ala Met Val Gln Glu Leu Thr
167 145 150 155 160
170 Asp His Gly Ile Glu His Cys Cys Leu Trp Gln Arg Gly Val Asp Thr
171 165 170 175
174 Glu Thr Phe Arg Pro Asp Leu Ala Thr Ala Ala Met Arg Asp Arg Leu
175 180 185 190
178 Ser Gly Gly Lys Pro Thr Ala Pro Leu Leu Leu Tyr Val Gly Arg Leu
179 195 200 205
182 Ser Ala Glu Lys Gln Ile Asp Arg Leu Arg Pro Ile Leu Asp Ala Asn
183 210 215 220
186 Pro Glu Ala Cys Leu Ala Leu Val Gly Asp Gly Pro His Arg Ala Glu
187 225 230 235 240
190 Leu Glu Gln Leu Phe Ala Gly Thr Gln Thr Gln Phe Ile Gly Tyr Leu
191 245 250 255
194 His Gly Glu Gln Leu Gly Ala Ala Tyr Ala Ser Ala Asp Ala Phe Val
195 260 265 270
198 Phe Pro Ser Arg Thr Glu Thr Leu Gly Leu Val Leu Leu Glu Ala Met
199 275 280 285
202 Ala Ala Gly Cys Pro Val Val Ala Ala Asn Ser Gly Gly Ile Pro Asp
203 290 295 300
206 Ile Val Ser Asp Gly Ile Asn Gly Phe Leu Phe Asp Pro Glu Asp Glu
207 305 310 315 320
210 Gln Gly Ala Ile Ala Ala Ile Gln Arg Leu Leu Ala Asn Pro Ala Glu
211 325 330 335
214 Arg Glu Ile Leu Arg Gln Ala Ala Arg Gln Glu Ala Glu Arg Trp Ser
215 340 345 350
218 Trp Asn Ala Ala Thr Arg Gln Leu Gln Asp Tyr Tyr Cys Glu Val Leu
219 355 360 365

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223 370 375

226 &lt;210&gt; SEQ ID NO: 3

227 &lt;211&gt; LENGTH: 2979

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236 ctttgctggt gctgctctcc aatcatatct ctcggtctct tctcttgccg cttttccaat      180
238 gatctctctt gtttcacggt cgtgcagtaa agttctcagt tttgtcacgc aatcttcaac      240
240 atctccaggg ttgaacaaaa atccggtttt tccctcctga tgaaaacatc agaatcagaa      300
242 aaccacaagc tcaatatagg ttgaccata agaacaatca atgcaagatc attttgtgta      360
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RAW SEQUENCE LISTING ERROR SUMMARY  
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**Invalid Line Length:**

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 7

**VERIFICATION SUMMARY**

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**DATE: 04/11/2007**

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**Input Set : A:\ES.txt**

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**L:12 M:270 C: Current Application Number differs, Replaced Current Application No**

**L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date**